SEQUENCE LISTING
<110>   Korea Research Institute of Bioscience and Biotechnology
         CHOI, Inpyo
         KANG, Hyung-Sik
         YOON, Suk-Ran
         KIM, Eun-Mi

<120>   Differentiation regulating agent containing gene which regulating
         differentiation from stem cells to natural killer cells as
         effective ingredient

<130>   58049-00034

<140>   US 10/597,305
         2006-07-19

<150>   PCT/KR2005/000188
         2005-01-20

<150>   KR 10-2004-0004308
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<400>      9
ggcaacgaga agatcaccat
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<210>      11
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agggaacaga gctgactcca
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<400>      19
gaagaaagtg cctcaccagc
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<400>    27
gaccgagatg atgtggctct
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aaaagatgaa ggcagcctga
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<400> 31
gcagcaacct agaagccatc
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<210> 32
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<400> 32
tgtgagacgg caagaatgag
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<210> 33
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<400> 33
ttcaacctca cagagacccc
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<210> 34
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<400> 34
gtaagcttgc ttccacctgc
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gccagaaact ggaagcgtag
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<400>      36
ggtcacgaaa ctctgaagcc
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<210>      37
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<400>      37
gaatctgagc cgtaaggacg
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<400>      38
ctgcataaag ccggactagc
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<210>      39
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aagccaccta gagcgatttg
20
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34
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36
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gtcacgtcga agtacttggt g
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<400>      44
aaccagccac atagcacaca t
21


<210>      45
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<400>      45
gtggggcgcc ccaggcacca
20


<210>      46
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<400>      46
ctccttaatg tcacgcacga tttc
24


<210>      47
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Met Glu Ser Lys Ala Leu Leu Leu Val Val Leu Gly Val Trp Leu Gln
 1               5                  10                  15


agt ttg acc gcc ttc cga gga ggg gtg gcc gca gca gac gca gga aga
96
Ser Leu Thr Ala Phe Arg Gly Gly Val Ala Ala Ala Asp Ala Gly Arg
                20                  25                  30


gat ttc tca gac atc gaa agc aaa ttt gcc cta agg acc cct gaa gac
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144

Asp Phe Ser Asp Ile Glu Ser Lys Phe Ala Leu Arg Thr Pro Glu Asp
     35   40   45

aca gct gag gac act tgt cat ctc att cct gga tta gca gac tct gtg
192
Thr Ala Glu Asp Thr Cys His Leu.Ile Pro Gly Leu Ala Asp Ser Val
    50   55   60

tct aac tgc cac ttc aac cac agc agc aag acc ttc gtg gtg atc cat
240
Ser Asn Cys His Phe Asn His Ser Ser Lys Thr Phe Val Val Ile His
 65   70   75   80

gga tgg acg gta acg gga atg tat gag agt tgg gtg ccc aaa ctt gtg
288
Gly Trp Thr Val Thr Gly Met Tyr Glu Ser Trp Val Pro Lys Leu Val
            85   90   95

gcc gcc ctg tac aag aga gaa cct gac tcc aat gtc att gta gta gac
336
Ala Ala Leu Tyr Lys Arg Glu Pro Asp Ser Asn Val Ile Val Val Asp
          100   105   110

tgg ttg tat cgg gcc cag caa cat tat cca gtg tca gct ggc tac acc
384
Trp Leu Tyr Arg Ala Gln Gln His Tyr Pro Val Ser Ala Gly Tyr Thr
         115   120   125

aag ctg gtg gga aat gat gtg gcc aga ttc atc aac tgg atg gag gag
432
Lys Leu Val Gly Asn Asp Val Ala Arg Phe Ile Asn Trp Met Glu Glu
    130   135   140

gag ttt aag tac ccc cta gac aac gtc cac ctc tta ggg tac agc ctt
480
Glu Phe Lys Tyr Pro Leu Asp Asn Val His Leu Leu Gly Tyr Ser Leu
145   150   155   160

gga gcc cat gct gct ggc gta gca gga agt ctg acc aat aag aag gtc
528
Gly Ala His Ala Ala Gly Val Ala Gly Ser Leu Thr Asn Lys Lys Val
         165   170   175

aat aga att act ggt ttg gat cca gct ggg cct aac ttt gag tat gca
576
Asn Arg Ile Thr Gly Leu Asp Pro Ala Gly Pro Asn Phe Glu Tyr Ala
         180   185   190

gaa gcc ccc agt cgc ctt tct cct gat gac gct gat ttt gta gat gtc
624
Glu Ala Pro Ser Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val
         195   200   205

tta cac aca ttt acc agg ggg tca cct ggt cga agt att ggg atc cag
672
Leu His Thr Phe Thr Arg Gly Ser Pro Gly Arg Ser Ile.Gly Ile Gln
    210   215   220

aaa cca gtg ggg cat gtt gac att tat ccc aat gga ggc act ttc cag
720
Lys Pro Val Gly His Val Asp Ile Tyr Pro Asn Gly Gly Thr Phe Gln
225   230   235   240

cca gga tgc aac att gga gaa gcc atc cgt gtg att gca gag aga gga
768
Pro Gly Cys Asn Ile Gly Glu Ala Ile Arg Val Ile Ala Glu Arg Gly
            245   250   255

ctc gga gac gtg gac cag ctg gtg aag tgc tcg cat gag cgc tcc att
816
Leu Gly Asp Val Asp Gln Leu Val Lys Cys Ser His Glu Arg Ser Ile
            260   265   270

cat ctc ttc att gac tcc ctg ctg aat gaa gaa aac ccc agc aaa gca
864
His Leu Phe Ile Asp Ser Leu Leu Asn Glu Glu Asn Pro Ser Lys Ala
        275   280   285

tac agg tgc aac tcc aag gaa gcc ttt gag aaa ggg ctc tgc ctg agt
912
Tyr Arg Cys Asn Ser Lys Glu Ala Phe Glu Lys Gly Leu Cys Leu Ser
        290   295   300

tgt aga aag aat cgc tgt aac aat ctg ggc tat gag atc aac aag gtc
960
Cys Arg Lys Asn Arg Cys Asn Asn Leu Gly Tyr Glu Ile Asn Lys Val
305   310   315   320

aga gcc aag aga agc agc aag atg tac ctg aag act cgc tct cag atg
1008
Arg Ala Lys Arg Ser Ser Lys Met Tyr Leu Lys Thr Arg Ser Gln Met
            325   330   335

ccc tac aaa gtg ttc cat tac caa gtc aag att cac ttt tct ggg act
1056
Pro Tyr Lys Val Phe His Tyr Gln Val Lys Ile His Phe Ser Gly Thr
            340   345   350

gag aat ggc aag caa cac aac cag gcc ttc gaa att tct ctg tac ggc
1104
Glu Asn Gly Lys Gln His Asn Gln Ala Phe Glu Ile Ser Leu Tyr Gly
            355   360   365

aca gtg gcc gag agc gag aac att ccc ttc acc ctg ccc gag gtt tcc
1152
Thr Val Ala Glu Ser Glu Asn Ile Pro Phe Thr Leu Pro Glu Val Ser
        370   375   380

aca aat aaa acc tac tcc ttc ttg att tac acg gag gtg gac atc gga
1200
Thr Asn Lys Thr Tyr Ser Phe Leu Ile Tyr Thr Glu Val Asp Ile Gly
385   390   395   400

gaa ctg ctc atg atg aag ctt aag tgg atg agc gac tcc tac ttc agc
1248
Glu Leu Leu Met Met Lys Leu Lys Trp Met Ser Asp Ser Tyr Phe Ser
            405   410   415

tgg ccc gac tgg tgg agc agc ccc agc ttc gtc atc gag agg atc cga
1296
Trp Pro Asp Trp Trp Ser Ser Pro Ser Phe Val Ile Glu Arg Ile Arg
            420   425   430

gtg aaa gcc gga gag act cag aaa aag gtc atc ttc tgt gct agg gag
1344

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Val Lys Ala Gly Glu Thr Gln Lys Lys Val Ile Phe Cys Ala Arg Glu
        435                 440                 445

aaa gtt tct cat ctg cag aag gga aag gac tca gca gtg ttt gtg aaa
1392
Lys Val Ser His Leu Gln Lys Gly Lys Asp Ser Ala Val Phe Val Lys
        450                 455                 460

tgc cat gac aag tct ctg aag aag tct ggc         tga
1425
Cys His Asp Lys Ser Leu Lys Lys Ser Gly
465                 470
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<213>  Mus musculus
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Ser Leu Thr Ala Phe Arg Gly Gly Val Ala Ala Ala Asp Ala Gly Arg
        20              25              30

Asp Phe Ser Asp Ile Glu Ser Lys Phe Ala Leu Arg Thr Pro Glu Asp
        35              40              45

Thr Ala Glu Asp Thr Cys His Leu Ile Pro Gly Leu Ala Asp Ser Val
    50              55              60

Ser Asn Cys His Phe Asn His Ser Ser Lys Thr Phe Val Val Ile His
65              70              75              80

Gly Trp Thr Val Thr Gly Met Tyr Glu Ser Trp Val Pro Lys Leu Val
            85              90                  95

Ala Ala Leu Tyr Lys Arg Glu Pro Asp Ser Asn Val Ile Val Val Asp
        100             105             110

Trp Leu Tyr Arg Ala Gln Gln His Tyr Pro Val Ser Ala Gly Tyr Thr
        115             120             125

Lys Leu Val Gly Asn Asp Val Ala Arg Phe Ile Asn Trp Met Glu Glu
        130             135             140

Glu Phe Lys Tyr Pro Leu Asp Asn Val His Leu Leu Gly Tyr Ser Leu
145             150             155             160

Gly Ala His Ala Ala Gly Val Ala Gly Ser Leu Thr Asn Lys Lys Val
            165             170             175

Asn Arg Ile Thr Gly Leu Asp Pro Ala Gly Pro Asn Phe Glu Tyr Ala
        180             185             190

Glu Ala Pro Ser Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val
        195             200             205

Leu His Thr Phe Thr Arg Gly Ser Pro Gly Arg Ser Ile Gly Ile Gln
    210             215             220

Lys Pro Val Gly His Val Asp Ile Tyr Pro Asn Gly Gly Thr Phe Gln
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          Pro Gly Cys Asn Ile Gly Glu Ala Ile Arg Val Ile Ala Glu Arg Gly
                          245                 250                 255

          Leu Gly Asp Val Asp Gln Leu Val Lys Cys Ser His Glu Arg Ser Ile
                          260                 265                 270

          His Leu Phe Ile Asp Ser Leu Leu Asn Glu Glu Asn Pro Ser Lys Ala
                          275                 280                 285

          Tyr Arg Cys Asn Ser Lys Glu Ala Phe Glu Lys Gly Leu Cys Leu Ser
              290                 295                 300

          Cys Arg Lys Asn Arg Cys Asn Asn Leu Gly Tyr Glu Ile Asn Lys Val
          305                 310                 315                 320

          Arg Ala Lys Arg Ser Ser Lys Met Tyr Leu Lys Thr Arg Ser Gln Met
                          325                 330                 335

          Pro Tyr Lys Val Phe His Tyr Gln Val Lys Ile His Phe Ser Gly Thr
                          340                 345                 350

          Glu Asn Gly Lys Gln His Asn Gln Ala Phe Glu Ile Ser Leu Tyr Gly
                          355                 360                 365

          Thr Val Ala Glu Ser Glu Asn Ile Pro Phe Thr Leu Pro Glu Val Ser
              370                 375                 380

          Thr Asn Lys Thr Tyr Ser Phe Leu Ile Tyr Thr Glu Val Asp Ile Gly
          385                 390                 395                 400

          Glu Leu Leu Met Met Lys Leu Lys Trp Met Ser Asp Ser Tyr Phe Ser
                          405                 410                 415

          Trp Pro Asp Trp Trp Ser Ser Pro Ser Phe Val Ile Glu Arg Ile Arg
                          420                 425                 430

          Val Lys Ala Gly Glu Thr Gln Lys Lys Val Ile Phe Cys Ala Arg Glu
                          435                 440                 445

          Lys Val Ser His Leu Gln Lys Gly Lys Asp Ser Ala Val Phe Val Lys
              450                 455                 460

          Cys His Asp Lys Ser Leu Lys Lys Ser Gly
          465                 470
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1

1